

125  
C3

- 1 -

SEQUENCE LISTING

<110> LAU, Lester F.

<120> EXTRACELLULAR MATRIX SIGNALING MOLECULES

<130> 28758/36072

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<150> 09/142,569

<151> 1999-04-02

<150> 60/013,958

<151> 1996-03-15

<160> 32

<170> PatentIn Ver. 2.0

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<211> 1480

<212> DNA

<213> Mus musculus

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<221> CDS

<222> (180)..(1316)

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<223> Mouse cyr61 cDNA coding sequence

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- 2 -

aaggacaccc gccgcctcgg ccctcgcttc accgcactcc gggcgcatth gatcccgtg  
120

ctcgccggct tgttggttct gtgtcgccgc gctcgccccg gttcttctg cgcgccaca  
179

atg agc tcc agc acc ttc agg acg ctc gct gtc gcc gtc acc ctt ctc  
227

Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu  
1 5 10 15

cac ttg acc aga ctg gcg ctc tcc acc tgc ccc gcc gcc tgc cac tgc  
275

His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys  
20 25 30

cct ctg gag gca ccc aag tgc gcc ccg gga gtc ggg ttg gtc cgg gac  
323

Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp  
35 40 45

ggc tgc ggc tgc tgt aag gtc tgc gct aaa caa ctc aac gag gac tgc  
371

Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys  
50 55 60

agc aaa act cag ccc tgc gac cac acc aag ggg ttg gaa tgc aat ttc  
419

Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe  
65 70 75 80

ggc gcc agc tcc acc gct ctg aaa ggg atc tgc aga gct cag tca gaa  
467

Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu  
85 90 95

ggc aga ccc tgt gaa tat aac tcc aga atc tac caa aac ggg gaa agc  
515

- 3 -

Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser  
100 105 110

ttc cag ccc aac tgt aaa cac cag tgc aca tgt att gat ggc gcc gtg  
563

Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val  
115 120 125

ggc tgc att cct ctg tgt ccc caa gaa ctg tct ctc ccc aat ctg ggc  
611

Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly  
130 135 140

tgt ccc aac ccc cgg ctg gtg aaa gtc agc ggg cag tgc tgt gaa gag  
659

Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu  
145 150 155 160

tgg gtt tgt gat gaa gac agc att aag gac tcc ctg gac gac cag gat  
707

Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp  
165 170 175

gac ctc ctc gga ctc gat gcc tcg gag gtg gag tta acg aga aac aat  
755

Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn  
180 185 190

gag tta atc gca att gga aaa ggc agc tca ctg aag agg ctt cct gtc  
803

Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val  
195 200 205

ttt ggc acc gaa ccg cga gtt ctt ttc aac cct ctg cac gcc cat ggc  
851

Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly  
210 215 220

- 4 -

cag aaa tgc atc gtt cag acc acg tct tgg tcc cag tgc tcc aag agc  
899

Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser  
225 230 235 240

tgc gga act ggc atc tcc aca cga gtt acc aat gac aac cca gag tgc  
947

Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys  
245 250 255

cgc ctg gtg aaa gag acc cgg atc tgt gaa gtg cgt cct tgt gga caa  
995

Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln  
260 265 270

cca gtg tac agc agc cta aaa aag ggc aag aaa tgc agc aag acc aag  
1043

Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys  
275 280 285

aaa tcc cca gaa cca gtc aga ttt act tat gca gga tgc tcc agt gtc  
1091

Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val  
290 295 300

aag aaa tac cgg ccc aaa tac tgc ggc tcc tgc gta gat ggc cgg tgc  
1139

Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys  
305 310 315 320

tgc aca cct ctg cag acc aga act gtg aag atg cgg ttc cga tgc gaa  
1187

Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu  
325 330 335

gat gga gag atg ttt tcc aag aat gtc atg atg atc cag tcc tgc aaa  
1235

- 5 -

Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys  
340 345 350

tgt aac tac aac tgc ccg cat ccc aac gag gca tcg ttc cga ctg tac  
1283

Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr  
355 360 365

agc cta ttc aat gac atc cac aag ttc agg gac taagtgcctc cagggttcc  
1336

Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp

370

375

agtgtgggct ggacagagga gaagcgcaag catcatggag acgtgggtgg gcggaggatg  
1396

aatggtgcct tgctcattct tgagtagcat tagggtatctt caaaactgcc aaggggctga  
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tgtggacgga cagcagcgca gccg  
1480

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<212> PRT

<213> Mus musculus

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- 6 -

20

25

30

Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp

35

40

45

Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys

50

55

60

Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe

65

70

75

80

Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu

85

90

95

Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser

100

105

110

Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val

115

120

125

Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly

130

135

140

- 7 -

Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu

145 150 155 160

Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp

165 170 175

Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn

180 185 190

Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val

195 200 205

Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly

210 215 220

Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser

225 230 235 240

Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys

245 250 255

Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln

260 265 270

- 8 -

Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys

275

280

285

Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val

290

295

300

Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys

305

310

315

320

Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu

325

330

335

Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys

340

345

350

Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr

355

360

365

Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp

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<210> 3

<211> 1418

<212> DNA



<213> Homo sapiens

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<221> CDS

<222> (124)..(1266)

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120

aca atg agc tcc cgc atc gcc agg gcg ctc gcc tta gtc gtc acc ctt  
168

Met	Ser	Ser	Arg	Ile	Ala	Arg	Ala	Leu	Ala	Leu	Val	Val	Thr	Leu
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ctc cac ttg acc agg ctg gcg ctc tcc acc tgc ccc gct gcc tgc cac  
216

Leu	His	Leu	Thr	Arg	Leu	Ala	Leu	Ser	Thr	Cys	Pro	Ala	Ala	Cys	His
				20				25						30	

tgc ccc ctg gag gcg ccc aag tgc gcg ccg gga gtc ggg ctg gtc cgg  
264

Cys	Pro	Leu	Glu	Ala	Pro	Lys	Cys	Ala	Pro	Gly	Val	Gly	Leu	Val	Arg
				35				40					45		

gac ggc tgc ggc tgc tgt aag gtc tgc gcc aag cag ctc aac gag gac  
312

Asp	Gly	Cys	Gly	Cys	Cys	Lys	Val	Cys	Ala	Lys	Gln	Leu	Asn	Glu	Asp
				50				55				60			

tgc agc aaa acg cag ccc tgc gac cac acc aag ggg ctg gaa tgc aac  
360

- 10 -

Cys Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn  
65 70 75

ttc ggc gcc agc tcc acc gct ctg aag ggg atc tgc aga gct cag tca  
408

Phe Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser  
80 85 90 95

gag ggc aga ccc tgt gaa tat aac tcc aga atc tac caa aac ggg gaa  
456

Glu Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu  
100 105 110

agt ttc cag ccc aac tgt caa cat cag tgc aca tgt att gat ggc gcc  
504

Ser Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala  
115 120 125

gtg ggc tgc att cct ctg tgt ccc caa gaa cta tct ctc ccc aac ttg  
552

Val Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu  
130 135 140

ggc tgt ccc aac cct cgg ctg gtc aaa gtt acc ggg cag tgc tgc gag  
600

Gly Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu  
145 150 155

gag tgg gtc tgt gac gag gat agt atc aag gac ccc atg gag gac cag  
648

Glu Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln  
160 165 170 175

gac ggc ctc ctt ggc aag gag ctg gga ttc gat gcc tcc gag gtg gag  
696

Asp Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu  
180 185 190

- 11 -

ttg acg aga aac aat gaa ttg att gca gtt gga aaa ggc aga tca ctg  
744

Leu Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu  
195 200 205

aag cgg ctc cct gtt ttt gga atg gag cct cgc atc cta tac aac cct  
792

Lys Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro  
210 215 220

tta caa ggc cag aaa tgt att gtt caa aca act tca tgg tcc cag tgc  
840

Leu Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys  
225 230 235

tca aag acc tgt gga act ggt atc tcc aca cga gtt acc aat gac aac  
888

Ser Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn  
240 245 250 255

cct gag tgc cgc ctt gtg aaa gaa acc cgg att tgt gag gtg cgg cct  
936

Pro Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro  
260 265 270

tgt gga cag cca gtg tac agc agc ctg aaa aag ggc aag aaa tgc agc  
984

Cys Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser  
275 280 285

aag acc aag aaa tcc ccc gaa cca gtc agg ttt act tac gct gga tgt  
1032

Lys Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys  
290 295 300

ttg agt gtg aag aaa tac cgg ccc aag tac tgc ggt tcc tgc gtg gac  
1080

- 12 -

Leu Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp  
305 310 315

ggc cga tgc tgc acg ccc cag ctg acc agg act gtg aag atg cgg ttc  
1128

Gly Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe  
320 325 330 335

cgc tgc gaa gat ggg gag aca ttt tcc aag aac gtc atg atg atc cag  
1176

Arg Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln  
340 345 350

tcc tgc aaa tgc aac tac aac tgc ccg cat gcc aat gaa gca gcg ttt  
1224

Ser Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe  
355 360 365

ccc ttc tac agg ctg ttc aat gac att cac aaa ttt agg gac  
1266

Pro Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp  
370 375 380

taaatgctac ctgggtttcc agggcacacc tagacaaaca agggagaaga gtgtcagaat  
1326

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<212> PRT

<213> Homo sapiens

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His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys

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25

30

Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp

35

40

45

Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys

50

55

60

Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe

65

70

75

80

Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu

85

90

95

Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser

100

105

110

Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala Val

115

120

125

- 14 -

Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly

130

135

140

Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu Glu

145

150

155

160

Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln Asp

165

170

175

Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu Leu

180

185

190

Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu Lys

195

200

205

Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro Leu

210

215

220

Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser

225

230

235

240

Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro

245

250

255

- 15 -

Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys

260

265

270

Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys

275

280

285

Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Leu

290

295

300

Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly

305

310

315

320

Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe Arg

325

330

335

Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln Ser

340

345

350

Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe Pro

355

360

365

Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp

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375

380

<210> 5

<211> 2267

<212> DNA

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<222> (138)..(1181)

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120

cctaccgcgt cccgatac atg ctc gcc tcc gtc gca ggt ccc atc agc ctc  
170

Met Leu Ala Ser Val Ala Gly Pro Ile Ser Leu  
1 5 10

gcc ttg gtg ctc ctc gcc ctc tgc acc cgg cct gct acg ggc cag gac  
218

Ala Leu Val Leu Leu Ala Leu Cys Thr Arg Pro Ala Thr Gly Gln Asp  
15 20 25

tgc agc gcg caa tgt cag tgc gca gcc gaa gca gcg ccg cac tgc ccc  
266

Cys Ser Ala Gln Cys Gln Cys Ala Ala Glu Ala Ala Pro His Cys Pro  
30 35 40

gcc ggc gtg agc ctg gtg ctg gac ggc tgc ggc tgc tgc cgc gtc tgc  
314

Ala Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys  
45 50 55



- 17 -

gcc aag cag ctg gga gaa ctg tgt acg gag cgt gac ccc tgc gac cca  
362

Ala Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro  
60 65 70 75

cac aag ggc ctc ttc tgc gat ttc ggc tcc ccc gcc aac cgc aag att  
410

His Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile  
80 85 90

gga gtg tgc act gcc aaa gat ggt gca ccc tgt gtc ttc ggt ggg tcg  
458

Gly Val Cys Thr Ala Lys Asp Gly Ala Pro Cys Val Phe Gly Gly Ser  
95 100 105

gtg tac cgc agc ggt gag tcc ttc caa agc agc tgc aaa tac caa tgc  
506

Val Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys  
110 115 120

act tgc ctg gat ggg gcc gtg ggc tgc gtg ccc cta tgc agc atg gac  
554

Thr Cys Leu Asp Gly Ala Val Gly Cys Val Pro Leu Cys Ser Met Asp  
125 130 135

gtg cgc ctg ccc agc cct gac tgc ccc ttc ccg aga agg gtc aag ctg  
602

Val Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu  
140 145 150 155

cct ggg aaa tgc tgc aag gag tgg gtg tgt gac gag ccc aag gac cgc  
650

Pro Gly Lys Cys Cys Lys Glu Trp Val Cys Asp Glu Pro Lys Asp Arg  
160 165 170

aca gca gtt ggc cct gcc cta gct gcc tac cga ctg gaa gac aca ttt  
698

Thr Ala Val Gly Pro Ala Leu Ala Tyr Arg Leu Glu Asp Thr Phe  
175 180 185

- 18 -

ggc cca gac cca act atg atg cga gcc aac tgc ctg gtc cag acc aca  
746

Gly Pro Asp Pro Thr Met Met Arg Ala Asn Cys Leu Val Gln Thr Thr  
190 195 200

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794

Glu Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg  
205 210 215

gtt acc aat gac aat acc ttc tgc aga ctg gag aag cag agc cgc ctc  
842

Val Thr Asn Asp Asn Thr Phe Cys Arg Leu Glu Lys Gln Ser Arg Leu  
220 225 230 235

tgc atg gtc agg ccc tgc gaa gct gac ctg gag gaa aac att aag aag  
890

Cys Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys  
240 245 250

ggc aaa aag tgc atc cgg aca cct aaa atc gcc aag cct gtc aag ttt  
938

Gly Lys Lys Cys Ile Arg Thr Pro Lys Ile Ala Lys Pro Val Lys Phe  
255 260 265

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986

Glu Leu Ser Gly Cys Thr Ser Val Lys Thr Tyr Arg Ala Lys Phe Cys  
270 275 280

ggg gtg tgc aca gac ggc cgc tgc tgc aca ccg cac aga acc acc act  
1034

Gly Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr  
285 290 295

ctg cca gtg gag ttc aaa tgc ccc gat ggc gag atc atg aaa aag aat  
1082

Leu Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Ile Met Lys Lys Asn

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1130

Met Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp  
320 325 330

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1178

Asn Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met  
335 340 345

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1231

Ala

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1291

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1471

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1651

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- 20 -

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1771

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1831

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1891

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1951

gaattgtgac ctgagtgact ctctgtcaga acaaacaaat gctgtgcagg tgataaagct  
2011

atgtattgga agtcagattt ctagtaggaa atgtgggtcaa atccctgttg gtgaacaaat  
2071

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2131

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2251

gaaaaaaaaag gaattc  
2267

<210> 6

<211> 348

<212> PRT

<213> Mus musculus

<400> 6

Met Leu Ala Ser Val Ala Gly Pro Ile Ser Leu Ala Leu Val Leu Leu

- 21 -

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Gln Cys Ala Ala Glu Ala Ala Pro His Cys Pro Ala Gly Val Ser Leu			
35	40	45	
Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu Gly			
50	55	60	
Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu Phe			
65	70	75	80
Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr Ala			
85	90	95	
Lys Asp Gly Ala Pro Cys Val Phe Gly Gly Ser Val Tyr Arg Ser Gly			
100	105	110	
Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp Gly			
115	120	125	

- 22 -

Ala Val Gly Cys Val Pro Leu Cys Ser Met Asp Val Arg Leu Pro Ser

130

135

140

Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys Cys

145

150

155

160

Lys Glu Trp Val Cys Asp Glu Pro Lys Asp Arg Thr Ala Val Gly Pro

165

170

175

Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro Thr

180

185

190

Met Met Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala Cys

195

200

205

Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn

210

215

220

Thr Phe Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro

225

230

235

240

Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile

- 23 -

245

250

255

Arg Thr Pro Lys Ile Ala Lys Pro Val Lys Phe Glu Leu Ser Gly Cys

260

265

270

Thr Ser Val Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr Asp

275

280

285

Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu Phe

290

295

300

Lys Cys Pro Asp Gly Glu Ile Met Lys Lys Asn Met Met Phe Ile Lys

305

310

315

320

Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe Glu

325

330

335

Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala

340

345

<210> 7

<211> 2075

<212> DNA

<213> Homo sapiens

<220>

<223> CTGF cDNA coding sequence

<220>

<221> CDS

<222> (130)..(1176)

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60

ccagcgctcc aggccccgcg ctccccgtc gccgccaccg cgccctccgc tccgcccgca  
120

gtgccaaacc atg acc gcc gcc agt atg ggc ccc gtc cgc gtc gcc ttc gtg  
171

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val  
1 5 10

gtc ctc ctc gcc ctc tgc agc cgg ccg gcc gtc ggc cag aac tgc agc  
219

Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser  
15 20 25 30

ggg ccg tgc cgg tgc ccg gac gag ccg gcg ccg cgc tgc ccg gcg ggc  
267

Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly  
35 40 45

gtg agc ctc gtg ctg gac ggc tgc ggc tgc tgc cgc gtc tgc gcc aag  
315

Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys  
50 55 60

cag ctg ggc gag ctg tgc acc gag cgc gac ccc tgc gac ccg cac aag  
363

Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys  
65 70 75



- 25 -

ggc ctc ttc tgt gac ttc ggc tcc ccg gcc aac cgc aag atc ggc gtg  
411

Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val  
80 85 90

tgc acc gcc aaa gat ggt gct ccc tgc atc ttc ggt ggt acg gtg tac  
459

Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr  
95 100 105 110

cgc agc gga gag tcc ttc cag agc agc tgc aag tac cag tgc acg tgc  
507

Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys  
115 120 125

ctg gac ggg gcg gtg ggc tgc atg ccc ctg tgc agc atg gac gtt cgt  
555

Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg  
130 135 140

ctg ccc agc cct gac tgc ccc ttc ccg agg agg gtc aag ctg ccc ggg  
603

Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly  
145 150 155

aaa tgc tgc gag gag tgg gtg tgt gac gag ccc aag gac caa acc gtg  
651

Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val  
160 165 170

gtt ggg cct gcc ctc gcg gct tac cga ctg gaa gac acg ttt ggc cca  
699

Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro  
175 180 185 190

gac cca act atg att aga gcc aac tgc ctg gtc cag acc aca gag tgg  
747

Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp  
195 200 205

- 26 -

agc gcc tgt tcc aag acc tgt ggg atg ggc atc tcc acc cgg gtt acc  
795

Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr  
210 215 220

aat gac aac gcc tcc tgc agg cta gag aag cag agc cgc ctg tgc atg  
843

Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met  
225 230 235

gtc agg cct tgc gaa gct gac ctg gaa gag aac att aag aag ggc aaa  
891

Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys  
240 245 250

aag tgc atc cgt act ccc aaa atc tcc aag cct atc aag ttt gag ctt  
939

Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu  
255 260 265 270

tct ggc tgc acc agc atg aag aca tac cga gct aaa ttc tgt gga gta  
987

Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val  
275 280 285

tgt acc gac ggc cga tgc tgc acc ccc cac aga acc acc acc ctg ccg  
1035

Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro  
290 295 300

gtg gag ttc aag tgc cct gac ggc gag gtc atg aag aag aac atg atg  
1083

Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met  
305 310 315

ttc atc aag acc tgt gcc tgc cat tac aac tgt ccc gga gac aat gac  
1131

1131  
1083  
1035  
987  
939  
891  
843  
795

- 27 -

Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp  
320 325 330

atc ttt gaa tcg ctg tac tac agg aag atg tac gga gac atg gca  
1176

Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala  
335 340 345

tgaagccaga gagtgagaga cattaactca ttagactgga acttgaactg attcacatct  
1236

catttttccg taaaaatgat ttcagtagca caagttatct aaatctgttt ttctaactgg  
1296

gggaaaagat tcccacccaa ttcaaaacat tgtgccatgt caaacaaata gtctatcttc  
1356

cccagacact ggtttgaaga atgttaagac ttgacagtgg aactacatta gtacacagca  
1416

ccagaatgta tattaagggtg tggctttagg agcagtggga gggtagccgc ccggttagta  
1476

tcacagatc gactcttata cgagtaatat gcctgctatt tgaagtgtaa ttgagaagga  
1536

aaatttttagc gtgctcactg acctgcctgt agccccagtg acagctagga tgtgcattct  
1596

ccagccatca agagactgag tcaagttggt ccttaagtca gaacagcaga ctcagctctg  
1656

acattctgat tcgaatgaca ctgttcagga atcggaatcc tgtcgattag actggacagc  
1716

ttgtggcaag tgaatttgcc tgtaacaagc cagatTTTTT aaaatttata ttgtaaatat  
1776

1176  
1296  
1356  
1416  
1476  
1536  
1596  
1656  
1716  
1776

tgtgtgtgtg tgtgtgtgtg tatatatata .tatatatgta cagttatcta agttaattta  
1836

aagttgtttg tgccttttta tttttgtttt taatgctttg atatttcaat gttagcctca  
1896

atttctgaac accataggta gaatgtaaag cttgtctgat cgttcaaagc atgaaatgga  
1956

tacttatatg gaaattctgc tcagatagaa tgacagtccg tcaaaacaga ttgtttgcaa  
2016

aggggaggca tcagtgtctt ggcaggctga tttctaggta ggaaatgtgg tagctcacg  
2075

<210> 8

<211> 349

<212> PRT

<213> Homo sapiens

<400> 8

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu

1 5 10 15

Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro

20 25 30

Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser

35 40 45

Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu

50

55

60

Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu

65

70

75

80

Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr

85

90

95

Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser

100

105

110

Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp

115

120

125

Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro

130

135

140

Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys

145

150

155

160

Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly

165

170

175

- 30 -

Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro

180

185

190

Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala

195

200

205

Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp

210

215

220

Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg

225

230

235

240

Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys

245

250

255

Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly

260

265

270

Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr

275

280

285

Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu

290

295

300

- 31 -

Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile

305

310

315

320

Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe

325

330

335

Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala

340

345

<210> 9

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 9

ggggatctgt gacgagccca aggac

25

<210> 10

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 10

gggaattcga ccaggcagtt ggctcg  
26

<210> 11

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 11

ggggatcctg tgatgaagac agcatt  
26

<210> 12

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 12

gggaattcaa cgatgcattt ctggcc  
26

<210> 13

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic  
peptide



- 33 -

<400> 13

Asp Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp

1

5

10

15

Cys Ser Lys Thr Gln

20

<210> 14

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic  
peptide

<400> 14

Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val Gly Cys

1

5

10

15

Ile Pro Leu Cys Pro

20

<210> 15

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic  
peptide

<400> 15

- 34 -

Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser Cys Gly

1

5

10

15

Thr Gly Ile Ser Thr Arg Val Thr

20

<210> 16

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic  
peptide

<400> 16

Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys Arg Leu Val Lys

1

5

10

15

Glu Thr Arg Ile Cys Glu Val Arg Pro Cys

20

25

<210> 17

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic  
peptide

<400> 17

- 35 -

Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys Cys Thr Pro Leu Gln

1

5

10

15

Thr Arg Thr Val Lys

20

<210> 18

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer fH1

<400> 18

gcggcatgca gcgcgaccgc gaaatcccca gaaccagtc

39

<210> 19

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer rH1

<400> 19

tcgcgctgca tgccgcgccc gcttttaggc tgctgtacac tg

42

<210> 20

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer fH2

<400> 20

gtcgcggcat acgcgccaa atactgcggc tc

32

<210> 21

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer rH2

<400> 21

gcgcgtatgc cgcgacactg gagcatcctg c

31

<210> 22

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: upstream PCR  
primer

<400> 22

cagaccacgt cttggtcc

18

<210> 23

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: downstream PCR  
primer

<400> 23

gaataggctg tacagtcgg

19

<210> 24

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 24

cacaacagaa gccaggaacc

20

<210> 25

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: lower PCR  
primer

<400> 25

gaggggacga cgacagtatc

20

<210> 26

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: upper PCR  
primer

<400> 26

caacggagcc aggggaggtg

20

<210> 27

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: lower  
wild-type PCR primer

<400> 27

cggcgacaca gaaccaacaa

20

<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: lower mutant  
PCR primer

<400> 28

gaggggacga cgacagtatc

20

<210> 29

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic  
peptide

<400> 29

His His Leu Gly Gly Ala Lys Gln Ala Gly Asp Val

1

5

10

<210> 30

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic  
peptide

<400> 30

Ser Leu Lys Ala Gly Ala Ala Cys Ser Ala Thr Ala Lys Ser Pro Glu

1

5

10

15

Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val Ala Ala Tyr Ala

20

25

30

Pro Lys Tyr Cys Gly

35

<210> 31

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic  
peptide

<400> 31

Gly Arg Gly Asp Ser Pro

1

5

<210> 32

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic  
peptide

<400> 32

Gly Arg Gly Glu Ser Pro

1

5